



RECEIVED 031502

MAR 2 2 2002

RECEIVED

#8

SEQUENCE LISTING TECH CENTER 1600/2900 MAR 2 1 2002

TECH CENTER 1600/2900

<110> Lechler, Robert I.
Dorling, Anthony

<120> IMMUNOSUPPRESSION BY BLOCKING T CELL CO-STIMULATION SIGNAL 2 (B7/CD28 INTERACTION)

<130> 2292/0H795

<140> US 09/674,462

<141> 2001-05-08

<150> PCT/ GB99/01350

<151> 1999-04-30

<160> 27

<170> PatentIn Ver. 2.1

<210> 1

<211> 223

<212> PRT

<213> Sus scrofa

<400> 1

Met Ala Cys Ser Gly Phe Arg Ser His Gly Ala Trp Leu Glu Leu Thr
1 5 10 15

Ser Arg Thr Trp Pro Cys Thr Ala Leu Phe Ser Leu Leu Phe Ile Pro
20 25 30

Val Phe Ser Lys Gly Met His Val Ala Gln Pro Ala Val Val Leu Ala
35 40 45

Asn Ser Arg Gly Val Ala Ser Phe Val Cys Glu Tyr Gly Ser Ala Gly
50 55 60

Lys Ala Ala Glu Val Arg Val Thr Val Leu Arg Arg Ala Gly Ser Gln
65 70 75 80

Met Thr Glu Val Cys Ala Ala Thr Tyr Thr Val Glu Asp Glu Leu Thr
85 90 95

Phe Leu Asp Asp Ser Thr Cys Thr Gly Thr Ser Thr Glu Asn Lys Val
100 105 110

Asn Leu Thr Ile Gln Gly Leu Arg Ala Val Asp Thr Gly Leu Tyr Ile
115 120 125

Cys Lys Val Glu Leu Leu Tyr Pro Pro Pro Tyr Tyr Val Gly Met Gly
 130 135 140
 Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser
 145 150 155 160
 Asp Phe Leu Leu Trp Ile Leu Ala Ala Val Ser Ser Gly Leu Phe Phe
 165 170 175
 Tyr Ser Phe Leu Ile Thr Ala Val Ser Leu Ser Lys Met Leu Lys Lys
 180 185 190
 Arg Ser Pro Leu Thr Thr Gly Val Tyr Val Lys Met Pro Pro Thr Glu
 195 200 205
 Pro Glu Cys Glu Lys Gln Phe Gln Pro Tyr Phe Ile Pro Ile Asn
 210 215 220

<210> 2
 <211> 672
 <212> DNA
 <213> Sus scrofa

<400> 2
 atggcttgct ctggattccg gagccatggg gcttggtctg agcttacttc taggacctgg 60
 ccctgtacag ctctgttttc tcttctcttc atccctgtct tctccaaagg gatgcacgtg 120
 gcccaacctg cagtagtgct ggccaacagc cggggtgttg ccagctttgt gtgtgagtat 180
 ggggtctgcag gcaaagctgc cgagggtccg gtgacagtgc tgcggcgggc cggcagccag 240
 atgactgaag tctgtgccgc gacatatact gtggaggatg agttgacctt ccttgatgac 300
 tctacatgca ctggcacctc caccgaaaac aaagtgaacc tcaccatcca agggctgaga 360
 gccgtggaca ctgggctcta catctgcaag gtggagctcc tgtaccacc accctactat 420
 gtgggtatgg gcaacgggac ccagatttat gtcattgatc cagaaccatg cccagattct 480
 gatttcctgc tctggatcct ggcagcagtt agttcagggt tgttttttta cagcttcctc 540
 atcacagctg tttctttgag caaaatgcta aagaaaagaa gtcctcttac tacaggggtc 600
 tatgtgaaaa tgccccgcac agagccagaa tgtgaaaagc aatttcagcc ttattttatt 660
 cccatcaatt ga 672

<210> 3
 <211> 400
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> pCTLA4-Ig construct (Figure 4)

<400> 3
 Met Ala Cys Ser Gly Phe Arg Ser His Gly Ala Trp Leu Glu Leu Thr
 1 5 10 15

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Arg | Thr | Trp | Pro | Cys | Thr | Ala | Leu | Phe | Ser | Leu | Leu | Phe | Ile | Pro |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Val | Phe | Ser | Lys | Gly | Met | His | Val | Ala | Gln | Pro | Ala | Val | Val | Leu | Ala |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Asn | Ser | Arg | Gly | Val | Ala | Ser | Phe | Val | Cys | Glu | Tyr | Gly | Ser | Ala | Gly |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Lys | Ala | Ala | Glu | Val | Arg | Val | Thr | Val | Leu | Arg | Arg | Ala | Gly | Ser | Gln |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 |
| Met | Thr | Glu | Val | Cys | Ala | Ala | Thr | Tyr | Thr | Val | Glu | Asp | Glu | Leu | Thr |
| | | | | 85 | | | | | 90 | | | | | 95 | |
| Phe | Leu | Asp | Asp | Ser | Thr | Cys | Thr | Gly | Thr | Ser | Thr | Glu | Asn | Lys | Val |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Asn | Leu | Thr | Ile | Gln | Gly | Leu | Arg | Ala | Val | Asp | Thr | Gly | Leu | Tyr | Ile |
| | | 115 | | | | | 120 | | | | | 125 | | | |
| Cys | Lys | Val | Glu | Leu | Leu | Tyr | Pro | Pro | Pro | Tyr | Tyr | Val | Gly | Met | Gly |
| | 130 | | | | | 135 | | | | | 140 | | | | |
| Asn | Gly | Thr | Gln | Ile | Tyr | Val | Ile | Asp | Pro | Glu | Pro | Cys | Pro | Asp | Ser |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 |
| Asp | Gly | Gly | Ser | Gly | Gly | Ala | Ala | Glu | Pro | Lys | Ser | Cys | Asp | Lys | Thr |
| | | | | 165 | | | | | 170 | | | | | 175 | |
| His | Thr | Cys | Pro | Pro | Cys | Pro | Ala | Pro | Glu | Leu | Leu | Gly | Gly | Pro | Ser |
| | | | 180 | | | | | 185 | | | | | 190 | | |
| Val | Phe | Leu | Phe | Pro | Pro | Lys | Pro | Lys | Asp | Thr | Leu | Met | Ile | Ser | Arg |
| | | 195 | | | | | 200 | | | | | 205 | | | |
| Thr | Pro | Glu | Val | Thr | Cys | Val | Val | Val | Asp | Val | Ser | His | Glu | Asp | Pro |
| | | 210 | | | | 215 | | | | | 220 | | | | |
| Glu | Val | Lys | Phe | Asn | Trp | Tyr | Val | Asp | Gly | Val | Glu | Val | His | Asn | Ala |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 |
| Lys | Thr | Lys | Pro | Arg | Glu | Glu | Gln | Tyr | Asn | Ser | Thr | Tyr | Arg | Val | Val |
| | | | | 245 | | | | | 250 | | | | | 255 | |
| Ser | Val | Leu | Thr | Val | Leu | His | Gln | Asp | Trp | Leu | Asn | Gly | Lys | Glu | Tyr |
| | | | 260 | | | | | 265 | | | | | 270 | | |
| Lys | Cys | Lys | Val | Ser | Asn | Lys | Ala | Leu | Pro | Ala | Pro | Ile | Glu | Lys | Thr |
| | | 275 | | | | | 280 | | | | | 285 | | | |

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
 290 295 300
 Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys
 305 310 315 320
 Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
 325 330 335
 Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
 340 345 350
 Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
 355 360 365
 Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
 370 375 380
 Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 385 390 395 400

<210> 4
 <211> 722
 <212> DNA
 <213> Phage library

<400> 4
 ccgaggtgca gctggtggag tctggggggag gcttggtaca gcctggggggg tccctgagac 60
 tctcctgtgc agcctctgga ttcaccttta gcagctatgc catgagctgg gtccgccagg 120
 ctccaggga ggggctggag tgggtctcag ctattcgtgg tagtggtggg agcacatact 180
 acgcagactc cgtgaagggc cggttcacca tctccagaga caattccaag aacacgctgt 240
 atctgcaaat gaacagcctg agagccgagg acacggccgt gtattactgt gcaagagctg 300
 gtcgtatddd gtttgactat tggggccaag gtaccctggg caccgtctcg agtggtggag 360
 gcggttcagg cggaggtggc tctggcggta gtgcacttca gtctgtgctg actcagccac 420
 cctcagcgtc tgggaccccc gggcagcggg tcaccatctc ttgttctgga agcagctcca 480
 acatcggaag taattatgta tactggtacc agcagctccc aggaacggcc cccaaactcc 540
 tcatctatag gaataatcag cggccctcag gggtccttga ccgattctct ggctccaagt 600
 ctggcacctc agcctccctg gccatcagtg ggctccgggtc cgaggatgag gctgattatt 660
 actgtgcagc atgggatgac agcctggtat tcggcggagg gaccaagctc accgtcctag 720
 gt 722

<210> 5
 <211> 240
 <212> PRT
 <213> Phage library

<400> 5

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Val | Gln | Leu | Val | Glu | Ser | Gly | Gly | Gly | Leu | Val | Gln | Pro | Gly | Gly |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Ser | Leu | Arg | Leu | Ser | Cys | Ala | Ala | Ser | Gly | Phe | Thr | Phe | Ser | Ser | Tyr |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Ala | Met | Ser | Trp | Val | Arg | Gln | Ala | Pro | Gly | Lys | Gly | Leu | Glu | Trp | Val |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Ser | Ala | Ile | Ser | Gly | Ser | Gly | Gly | Ser | Thr | Tyr | Tyr | Ala | Asp | Ser | Val |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Lys | Gly | Arg | Phe | Thr | Ile | Ser | Arg | Asp | Asn | Ser | Lys | Asn | Thr | Leu | Tyr |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 |
| Leu | Gln | Met | Asn | Ser | Leu | Arg | Ala | Glu | Asp | Thr | Ala | Val | Tyr | Tyr | Cys |
| | | | | 85 | | | | | 90 | | | | | 95 | |
| Ala | Arg | Ala | Gly | Arg | Ile | Leu | Phe | Asp | Tyr | Trp | Gly | Gln | Gly | Thr | Leu |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Val | Thr | Val | Ser | Ser | Gly | Gly | Gly | Gly | Ser | Gly | Gly | Gly | Gly | Ser | Gly |
| | | 115 | | | | | 120 | | | | | 125 | | | |
| Gly | Ser | Ala | Leu | Gln | Ser | Val | Leu | Thr | Gln | Pro | Pro | Ser | Ala | Ser | Gly |
| | 130 | | | | | 135 | | | | | 140 | | | | |
| Thr | Pro | Gly | Gln | Arg | Val | Thr | Ile | Ser | Cys | Ser | Gly | Ser | Ser | Ser | Asn |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 |
| Ile | Gly | Ser | Asn | Tyr | Val | Tyr | Trp | Tyr | Gln | Gln | Leu | Pro | Gly | Thr | Ala |
| | | | 165 | | | | | | 170 | | | | | 175 | |
| Pro | Lys | Leu | Leu | Ile | Tyr | Arg | Asn | Asn | Gln | Arg | Pro | Ser | Gly | Val | Pro |
| | | | 180 | | | | | 185 | | | | | 190 | | |
| Asp | Arg | Phe | Ser | Gly | Ser | Lys | Ser | Gly | Thr | Ser | Ala | Ser | Leu | Ala | Ile |
| | | 195 | | | | | 200 | | | | | 205 | | | |
| Ser | Gly | Leu | Arg | Ser | Glu | Asp | Glu | Ala | Asp | Tyr | Tyr | Cys | Ala | Ala | Trp |
| | 210 | | | | | 215 | | | | | 220 | | | | |
| Asp | Asp | Ser | Leu | Val | Phe | Gly | Gly | Gly | Thr | Lys | Leu | Thr | Val | Leu | Gly |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 |

<210> 6
 <211> 729
 <212> DNA
 <213> Phage library

<400> 6
 catggccgag gtgcagctgg tggagtctgg gggaggcttg gtacagcctg gggggtcctt 60
 gagactctcc tgtgcagcct ctggattcac ctttagcagc tatgccatga gctgggtccg 120
 ccaggctcca gggaaggggc tggagtgggt ctcagctatt agtggtagtg gtggtagcac 180
 atactacgca gactccgtga agggccggtt caccatctcc agagacaatt ccaagaacac 240
 gctgtatctg caaatgaaca gcctgagagc cgaggacacg gccgtgtatt actgtgcaag 300
 agctggctcg attttgtttg actattgggg ccaaggtacc ctggtcaccg tctcgagtgg 360
 tggaggcggg tcaggcggag gtggctctgg cggtagtgca cttcagtctg tgctgactca 420
 gccaccctca gcgtctggga cccccgggca gagggtcacc atctcttggt ctggaagcag 480
 ctccaacatc ggaagtaatt atgtatactg gtaccagcag ctcccaggaa cggcccccaa 540
 actcctcatc tataggaata atcagcggcc ctcaggggtc cctgaccgat tctctggctc 600
 caagtctggc acctcagcct ccttggccat cagtgggctc cggtcgagg atgaggctga 660
 ttattactgt gcagcatggg atgacagcct ggtattcggc ggagggacca agctgaccgt 720
 cctaggtgc 729

<210> 7
 <211> 738
 <212> DNA
 <213> Phage library

<400> 7
 catggccgag gtgcagctgc aggagtcggg cccaggactg gtgaagcctc gggagaccct 60
 gtccctcacc tgcactgtct ctgggtggctc cgtcagcagt ggtagttact ggagctggat 120
 ccggcagccc ccagggaagg gactggagtg gattgggtat atctattaca gtgggagcac 180
 caactacaac ccctccctca agagtcgagt caccatatca gtagacacgt ccaagaacca 240
 gttctccctg aagctgagct ctgtgaccgc tgcggacacg gccgtgtatt actgtgcaag 300
 aatgcggaag gataagtttg actattgggg ccaaggtacc ctggtcaccg tctcgagtgg 360
 tggaggcggg tcaggcggag gtggctctgg cggtagtgca cttcagtctg tgctgactca 420
 gccaccctca gcgtctggga cccccgggca gagggtcacc atctcttggt ctggaagcag 480
 ctccaacatc ggaagtaatt atgtatactg gtaccagcag ctcccaggaa cggcccccaa 540
 actcctcatc tataggaata atcagcggcc ctcaggggtc cctgaccgat tctctggctc 600
 caagtctggc acctcagcct ccttggccat cagtgggctc cggtcgagg atgaggctga 660
 ttattactgt gcagcatggg atgacagcct gtttgtattc ggcggaggga ccaagctgac 720
 cgtcctaggt gcggccgc 738

<210> 8
 <211> 739
 <212> DNA
 <213> Phage library

<400> 8
 catggccgag gtgcagctgg tgcagtctgg ggctgagtga agaggccggg ggcctcagtg 60
 aaggtttcct gcaaggcatc tggatacacc ttcaccagct actatatgca ctgggtgcga 120
 caggcccctg gacaagggct tgagtggatg ggaataatca accctagtgg tggtagcaca 180

| | | | | | | |
|------------|------------|-------------|------------|------------|------------|-----|
| caagctacgc | acagaagttc | cagggcagag | tcaccatgac | cagggacacg | tccacgagca | 240 |
| cagtctacat | ggagctgagc | agcctgagat | ctgaggacac | ggccgtgtat | tactgtgcaa | 300 |
| gaatggctcc | ctatgtgaat | acgcttgttt | tttggggcca | aggtaccctg | gtcaccgtct | 360 |
| cgagtgggtg | aggcggttca | ggcggagggtg | gctctggcgg | tagtgäactt | cagtctgtgc | 420 |
| tgactcagga | ccctgctgtg | tctgtggcct | tgggacagac | agtcaggatc | acatgccaa | 480 |
| taggagacag | cctcagaagc | tattatgcaa | gctggtacca | gcagaagcca | ggacaggccc | 540 |
| ctgtacttgt | catctatgg | aaaaacaacc | ggccctcagg | gatcccagac | cgattctctg | 600 |
| gctccagctc | aggaaacaca | gcttccttga | ccatcactgg | ggctcaggcg | gaagatgagg | 660 |
| ctgactatta | ctgtaactcc | cgggacagca | gtggttttac | tgtattcggc | ggagggacca | 720 |
| agctgaccgt | cctaggtgc | | | | | 739 |

```
<210> 9
<211> 729
<212> DNA
<213> Phage library
```

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| <400> | 9 | | | | | |
| catgggccca | ggtgcagctg | ttgcagtctg | cagcagaggt | gaaaaagccc | ggggagtctc | 60 |
| tgaagatctc | ctgtaagggg | tctggataca | gctttaccag | ctactggatc | ggctgggtgc | 120 |
| gccagatgcc | cgggaaaggc | ctggagtgga | tggggatcat | ctatcctggg | gactctgata | 180 |
| ccagatacag | cccgtccttc | caaggccagg | tcaccatctc | agccgacaag | tccatcagca | 240 |
| ccgcctacct | gcagtgagc | agcctgaagg | cctcggacac | ggcctgtat | tactgtgcaa | 300 |
| gattttcgtc | tggtggtttt | gactattggg | gccaaagtac | cctgggtcac | gtctcgagtg | 360 |
| gtggaggcgg | ttcaggcgga | ggtggctctg | gcggtagtgc | acttgacatc | cagttgaccc | 420 |
| agtctccatg | ttcctgtctg | catctgtagg | agacagagtc | accatcactt | gccgggccag | 480 |
| tcagggcatt | agcagttatt | tagcctggta | tcagcaaaaa | ccagggaag | cccctaagct | 540 |
| cctggtctat | gctgcatcca | ctttgcaaag | tggggtccca | tcaaggttca | gcggcagtg | 600 |
| atctgggaca | gaattcactc | tcacaatcag | cagcctgcag | cctgaagatt | ttgcaactta | 660 |
| ttactgtcaa | cagcttaata | gttaccgctt | gacgttcggc | caagggacca | agctggaaat | 720 |
| caaacgtqc | | | | | | 729 |

```
<210> 10
<211> 240
<212> PRT
<213> Phage library
```

```

<400> 10
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1          5          10          15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
          20          25          30
Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
          35          40          45
Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
          50          55          60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

```

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 65 | | | | | 70 | | | | | | 75 | | | | 80 |
| Leu | Gln | Met | Asn | Ser | Leu | Arg | Ala | Glu | Asp | Thr | Ala | Val | Tyr | Tyr | Cys |
| | | | | 85 | | | | | 90 | | | | | 95 | |
| Ala | Arg | Ala | Gly | Arg | Ile | Leu | Phe | Asp | Tyr | Trp | Gly | Gln | Gly | Thr | Leu |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Val | Thr | Val | Ser | Ser | Gly | Gly | Gly | Gly | Ser | Gly | Gly | Gly | Gly | Ser | Gly |
| | | 115 | | | | | | 120 | | | | | 125 | | |
| Gly | Ser | Ala | Leu | Gln | Ser | Val | Leu | Thr | Gln | Pro | Pro | Ser | Ala | Ser | Gly |
| | 130 | | | | | 135 | | | | | 140 | | | | |
| Thr | Pro | Gly | Gln | Arg | Val | Thr | Ile | Ser | Cys | Ser | Gly | Ser | Ser | Ser | Asn |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 |
| Ile | Gly | Ser | Asn | Tyr | Val | Tyr | Trp | Tyr | Gln | Gln | Leu | Pro | Gly | Thr | Ala |
| | | | | 165 | | | | | 170 | | | | | 175 | |
| Pro | Lys | Leu | Leu | Ile | Tyr | Arg | Asn | Asn | Gln | Arg | Pro | Ser | Gly | Val | Pro |
| | | | 180 | | | | | 185 | | | | | 190 | | |
| Asp | Arg | Phe | Ser | Gly | Ser | Lys | Ser | Gly | Thr | Ser | Ala | Ser | Leu | Ala | Ile |
| | | 195 | | | | | 200 | | | | | 205 | | | |
| Ser | Gly | Leu | Arg | Ser | Glu | Asp | Glu | Ala | Ser | Tyr | Tyr | Cys | Ala | Ala | Trp |
| | 210 | | | | | 215 | | | | | 220 | | | | |
| Asp | Asp | Ser | Leu | Val | Phe | Gly | Gly | Gly | Thr | Lys | Leu | Thr | Val | Leu | Gly |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 |

<210> 11
 <211> 246
 <212> PRT
 <213> Phage library

<400> 11
 Met Ala Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro
 1 5 10 15
 Ser Glu Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Val Ser
 20 25 30
 Ser Gly Ser Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly
 35 40 45

Leu Glu Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Asn Tyr Asn
 50 55 60
 Pro Ser Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn
 65 70 75 80
 Gln Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val
 85 90 95
 Tyr Tyr Cys Ala Arg Met Arg Lys Asp Lys Phe Asp Tyr Trp Gly Gln
 100 105 110
 Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
 115 120 125
 Gly Ser Gly Gly Ser Ala Leu Gln Ser Val Leu Thr Gln Pro Pro Ser
 130 135 140
 Ala Ser Gly Thr Pro Gly Gln Arg Val Thr Ile Ser Cys Ser Gly Ser
 145 150 155 160
 Ser Ser Asn Ile Gly Ser Asn Tyr Val Tyr Trp Tyr Gln Gln Leu Pro
 165 170 175
 Gly Thr Ala Pro Lys Leu Leu Ile Tyr Arg Asn Asn Gln Arg Pro Ser
 180 185 190
 Gly Val Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser
 195 200 205
 Leu Ala Ile Ser Gly Leu Arg Ser Glu Asp Glu Ala Asp Tyr Tyr Val
 210 215 220
 Ala Ala Trp Asp Asp Ser Leu Phe Val Phe Gly Gly Gly Thr Lys Leu
 225 230 235 240
 Thr Val Leu Gly Ala Ala
 245

<210> 12

<211> 242

<212> PRT

<213> Phage library

<400> 12

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Arg Pro Gly Ala
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
 20 25 30
 Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45
 Gly Ile Ile Asn Pro Ser Gly Gly Ser Thr Ser Tyr Ala Gln Lys Phe
 50 55 60
 Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
 65 70 75 80
 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Val Ala Pro Tyr Val Asn Thr Leu Val Phe Trp Gly Gln Gly
 100 105 110
 Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 115 120 125
 Ser Gly Gly Ser Ala Leu Ser Ser Glu Leu Thr Gln Asp Pro Ala Val
 130 135 140
 Ser Val Ala Leu Gly Gln Thr Val Arg Ile Thr Cys Gln Gly Asp Ser
 145 150 155 160
 Leu Arg Ser Tyr Tyr Ala Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala
 165 170 175
 Pro Val Leu Val Ile Tyr Gly Lys Asn Asn Arg Pro Ser Gly Ile Pro
 180 185 190
 Asp Arg Phe Ser Gly Ser Ser Ser Gly Asn Thr Ala Ser Leu Thr Ile
 195 200 205
 Thr Gly Ala Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Asn Ser Arg
 210 215 220
 Asp Ser Ser Gly Phe Thr Val Phe Gly Gly Gly Thr Lys Leu Thr Val
 225 230 235 240

Leu Gly

<210> 13

<211> 240

<212> PRT

<213> Phage library

<400> 13

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Val | Gln | Leu | Leu | Gln | Ser | Ala | Ala | Glu | Val | Lys | Lys | Pro | Gly | Glu |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Ser | Leu | Lys | Ile | Ser | Cys | Lys | Gly | Ser | Gly | Tyr | Ser | Phe | Thr | Ser | Tyr |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Trp | Ile | Gly | Trp | Val | Arg | Gln | Met | Pro | Gly | Lys | Gly | Leu | Glu | Trp | Met |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Gly | Ile | Ile | Tyr | Pro | Gly | Asp | Ser | Asp | Thr | Arg | Tyr | Ser | Pro | Ser | Phe |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Gln | Gly | Gln | Val | Thr | Ile | Ser | Ala | Asp | Lys | Ser | Ile | Ser | Thr | Ala | Tyr |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 |
| Leu | Gln | Trp | Ser | Ser | Leu | Lys | Ala | Ser | Asp | Thr | Ala | Val | Tyr | Tyr | Cys |
| | | | | 85 | | | | | 90 | | | | | 95 | |
| Ala | Arg | Phe | Ser | Leu | Gly | Gly | Phe | Asp | Tyr | Trp | Gly | Gln | Gly | Thr | Leu |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Val | Thr | Val | Ser | Ser | Gly | Gly | Gly | Gly | Ser | Gly | Gly | Gly | Gly | Ser | Gly |
| | | 115 | | | | | | 120 | | | | | 125 | | |
| Gly | Ser | Ala | Leu | Asp | Ile | Gln | Leu | Thr | Gln | Ser | Pro | Ser | Phe | Leu | Ser |
| | 130 | | | | | 135 | | | | | 140 | | | | |
| Ala | Ser | Val | Gly | Asp | Arg | Val | Thr | Ile | Thr | Cys | Arg | Ala | Ser | Gln | Gly |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 |
| Ile | Ser | Ser | Tyr | Leu | Ala | Trp | Tyr | Gln | Gln | Lys | Pro | Gly | Lys | Ala | Pro |
| | | | | 165 | | | | | 170 | | | | | 175 | |
| Lys | Leu | Leu | Val | Tyr | Ala | Ala | Ser | Thr | Leu | Gln | Ser | Gly | Val | Pro | Ser |
| | | | 180 | | | | | 185 | | | | | 190 | | |
| Arg | Phe | Ser | Gly | Ser | Gly | Ser | Gly | Thr | Glu | Phe | Thr | Leu | Thr | Ile | Ser |
| | | 195 | | | | | 200 | | | | | 205 | | | |
| Ser | Leu | Gln | Pro | Glu | Asp | Phe | Ala | Thr | Tyr | Tyr | Cys | Gln | Gln | Leu | Asn |
| | 210 | | | | | 215 | | | | | 220 | | | | |
| Ser | Tyr | Arg | Leu | Thr | Phe | Gly | Gln | Gly | Thr | Lys | Leu | Glu | Ile | Lys | Arg |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 |

<210> 14
 <211> 742
 <212> DNA
 <213> Homo sapiens

<400> 14
 agcttcagga tcctgaaagg ttttgctcta cttcctgaag acctgaacac cgctcccata 60
 aagccatggc ttgccttgga tttcagcggc acaagggtca gctgaacctg gctaccagga 120
 cctggccctg cactctcctg ttttttcttc tcttcatccc tgtcttctgc aaagcaatgc 180
 acgtggccca gcttgctgtg gtactggcca gcagccgagg catcgccagc tttgtgtgtg 240
 agtatgcac tccaggcaaa gccactgagg tccgggtgac agtgcttcgg caggctgaca 300
 gccagggtgac tgaagtctgt gcggcaacct acatgatggg gaatgagttg accttcctag 360
 atgattccat ctgcacgggc acctccagtg gaaatcaagt gaacctcact atccaaggac 420
 tgagggccat ggacacggga ctctacatct gcaagggtga gctcatgtac ccaccgccat 480
 actacctggg cataggcaac ggaaccagga tttatgtaat tgatccagaa ccgtgccag 540
 attctgactt cctcctctgg atccttgacag cagttagtctc ggggttggtt ttttatagct 600
 ttctcctcac agctgtttct ttgagcaaaa tgctaaagaa aagaagccct cttacaacag 660
 gggctctatgt gaaaatgccc ccaacagagc cagaatgtga aaagcaattt cagccttatt 720
 ttattcccat caattgagaa tt 742

<210> 15
 <211> 223
 <212> PRT
 <213> Homo sapiens

<400> 15
 Met Ala Cys Leu Gly Phe Gln Arg His Lys Ala Gln Leu Asn Leu Ala
 1 5 10 15
 Thr Arg Thr Trp Pro Cys Thr Leu Leu Phe Phe Leu Leu Phe Ile Pro
 20 25 30
 Val Phe Cys Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala
 35 40 45
 Ser Ser Arg Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly
 50 55 60
 Lys Ala Thr Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln
 65 70 75 80
 Val Thr Glu Val Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr
 85 90 95
 Phe Leu Asp Asp Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val
 100 105 110
 Asn Leu Thr Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile
 115 120 125

Cys Lys Val Glu Leu Met Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly
 130 135 140
 Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser
 145 150 155 160
 Asp Phe Leu Leu Trp Ile Leu Ala Ala Val Ser Ser Gly Leu Phe Phe
 165 170 175
 Tyr Ser Phe Leu Leu Thr Ala Val Ser Leu Ser Lys Met Leu Lys Lys
 180 185 190
 Arg Ser Pro Leu Thr Thr Gly Val Tyr Val Lys Met Pro Pro Thr Glu
 195 200 205
 Pro Glu Cys Glu Lys Gln Phe Gln Pro Tyr Phe Ile Pro Ile Asn
 210 215 220

<210> 16
 <211> 773
 <212> DNA
 <213> Homo sapiens

<400> 16
 aagcttcgag ccaagcagcg tcctgggggag cgcgtcatgg ccttaccagt gaccgccttg 60
 ctcttgccgc tggccttgct gctccacgcc gccaggccga gccagttccg ggtgtcgccg 120
 ctggatcgga cctggaacct gggcgagaca gtggagctga agtgccaggt gctgctgtcc 180
 aaccgcagct cgggctgctc gtggctcttc cagccgcgcg gcgccgccgc cagtcccacc 240
 ttctctctat acctctccca aaacaagccc aaggcggccg aggggctgga caccagcgcg 300
 ttctcgggca agaggttggg ggacaccttc gtctcacc ccgagcgactt ccgagagag 360
 aacgagggct actatttctg ctcggccctg agcaactcca tcatgtactt cagccacttc 420
 gtgccggtct tcttgccagc gaagcccacc acgacgccag cgccgcgacc accaacaccg 480
 gcgcccacca tcgcgtcgca gccctgtgcc ctgcgccag aggcgtgccg gccagcgccg 540
 gggggcgagc tgcacacgag ggggctggac ttgcgctgtg atatctacat ctgggcgccc 600
 ttggccggga cttgtggggg ccttctcctg tcaactgtta tcacccttta ctgcaaccac 660
 aggaaccgaa gacgtgtttg caaatgtccc cggcctgtgg tcaaatcggg agacaagccc 720
 agcctttcgg cgagatacgt ctaaccctgt gcaacagcca ctacatgaat tcc 773

<210> 17
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR primer

<400> 17
 ttgaagctta gccatggctt gctctgga

<210> 18
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 18
taatgaattc tcaattgatg ggaataaaat aag

33

<210> 19
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 19
cggttctgca gcaccaccgg agccaccatc agaatctggg catggttctg gatcaatgac 60

<210> 20
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 20
gagctgaaac gggcggccgc agaac

25

<210> 21
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 21
ctggcctgca gcattcagat cc

22

<210> 22
<211> 30
<212> DNA
<213> Artificial Sequence

<220>

<223> PCR primer

<400> 22

ttcaaagctt caggatcctg aaaggttttg

30

<210> 23

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 23

taatgaattc tcaattgatg ggaataaaat aag

33

<210> 24

<211> 76

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 24

gatgtagata tcacaggcga agtcgacacc accggagcca ccaattacat aaatctgggc 60
tccgttgcct atgccc 76

<210> 25

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 25

tcgcgcccga gcttcgagcc aagcagcgt

29

<210> 26

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 26

taatgaattc tcaattgatg ggaataaaaat aag

33

<210> 27

<211> 73

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 27

cataggcaac ggagcccaga tttatgtaat tgggtggctcc ggtggtgtcg acttcgcctg 60

tgatatctac atc

73